

Contents

- [1 What is the Gene Ontology?](#)
- [2 EVS Processing](#)
- [3 Discuss Gene Ontology Terminology](#)
- [4 Links](#)

What is the Gene Ontology?

The [Gene Ontology \(GO\)](#) project, run by the GO Consortium, is a collaborative effort to address the need for consistent descriptions of gene products in different databases. The GO collaborators are developing three structured, controlled vocabularies (ontologies) that describe gene products in terms of their associated biological processes, cellular components and molecular functions in a species-independent manner.

GO was the first external vocabulary to undergo review to become a caBIG approved terminology, and GO is an approved vocabulary for ?tagging? Common Data Elements (CDEs) through the [caDSR](#).

EVS Processing

EVS downloads the monthly OBO archive from the [Gene Ontology website](#) and loads it into the [LexBIG terminology server](#). It is then available through various API's and services, as well as through the [NCI Terminology Browser](#).

GO also provides a gene information structure within the [BiomedGT](#) vocabulary. BiomedGT is a federated terminology which imports the OWL format of the GO published data into the Protégé ontology editor. The EVS editors then build relationships and extensions to the GO data within the BiomedGT.

Discuss Gene Ontology Terminology

Please go to the [Gene Ontology Discussion](#) page to leave comments regarding the Gene Ontology Terminology.

Examples of comments may include:

- How you are using this terminology
- Why you decided to use (or not use) this terminology
- Strengths or limitations of the terminology
- Comparisons to other similar terminologies

Links

[Gene Ontology FAQ](#)

[Gene Ontology Home Page](#)